

FIGURE 1

GGACTAATCTGGGGAGCAGTTTATTCCAGTATCACCCAGGGTCAGGCCACACCAGGACTGT
GTTGAAGGGTGTCCCCCTTTAAATGTAATACCTCTCATCTTCTTACACAGTG
TCTGAGAACATTACATTAGATAAGTAGTACATGGGGATACTCTACTTTAGGAGGA
CTACTCTCTCTGACAGTCTAGACTGCTCTACACTAAAGACACCATGAAGGAGTATGTG
CTCCTATTCTCTGGCTTGTGCTCTGCCAACCCCTTCTTAGGCCCTCACACATCGCACT
GAAGAAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTCCAACAAAGAGGCCAAGAAGGCCATTCTTCA
TTTGATCTGTTTCCAATGTGCCATTGGATGTCAGTGTCTTACAGGTTGACATTGCTC
AGATTTAGGTTTGTACCTCAGTCCCACCAACATTCCATTGATACTCGAATGCTGATCTC
AAAACAATAAAATTAAAGGAATCAAAGAAAATGATTTAAAGGACTCACTTCACTTATGGT
CTGATCTGAAACACAACAGCTAACAGGAATTCAACCAAAAGCCTTCTAACCCAAAGAA
GTTGCAAGGGCTGTCTGTCACAACTCAACTAAGTGAATAACCACTTAACTTCCAAAT
CATTCAGCAGAACATGAAATTCTGAAAAAAATGAAAGTAAACAAAGGACACATTCAA
GGAATGAATGCTTACAGTTGGAAATGAGTGCACAAACCTCTTGATAATAATGGGATAGA
GCCAGGGGCTTGAAAGGGGTGACGGTGTCCATATCGAATTGCGAGAACAACTGACCT
CAGTTCTAAAGGCTTACACCAACTTTATGGAGCTTCACTTAGATTTAAATAAAATTCTA
ACAGTGGAACTTGGAGATTAAACAGTACAAAGAACATACAAAGGCTGGCCTAGGAAACAA
AAAATCACAGATCTGAAATGGAGTCTGCTAACATACACGTTGAGAGAAATACATT
TGGAAAACAATAAACTAAAAAAATCTCTTCAAGGATTACACAGAGTTGAAATCTCCAGATA
ATCTCTTCTTCAATTCTAAATTGCAAGAGTGGAGTAATGACTTCTGTCACAGTGCC
AAAGATGAAGAAATCTTATACAGTGCATAAAGTTTATCAACAAACCCGGTGAATACTGGG
AAATGCAACCTGCAACATTCTGTTGAGGAGTTCAGCTTGGAAACTT
GGAAT**TAA**TTAATTAGTAAATTGTAATGTCATTAAATAGATTCAAATCCTTACATT
TGGATAACTTGAACTCTATTAAATGTTGAGTATTATATACAGGAAATATCTTCA
AGTGGTAAGTCCACTGACTTATTTATGACAAGAAATTCAACGGAAATTGCGCAACTATT
GATACATAAGGGTTGAGAGAACAAAGCATCTTGTGAGTGGAGTGGAGTGGAGTGG
CTTACATAAACTCTGCTGACATTCTTCTTCAATAACAAAAAAAGTAAAGATATTGGTA
TTAACACCTTGTATCAAGCACATTAAAAGAACACTGACTGTAATGGAATGTTGACT
TAGCAAAATTGTCCTTCTTCAATTGCTGTTAGAAAACAGAATTAAACAAAGACATTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTAGTAACTGGTAGTACTGTAATTTTAAAT
CATCTTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGCTTAGGCCGT
CTTTATGTTAAAACAAATTCTTAAAGGAAATTGCGCTTCAAGTAAATGTTCATTACAACTTGA
TAAATGCTACTAACAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTAAATT
ACCTGATTAAACATCTGTAACAGCTGAGTGTCTTATCAAATCTGTAACCGCATTTT
AATGATCCGCTTAAAGCTTAAAGCATGAAATTGTTAGGCTATATAACATTGCCAC
TTCAACTCTAAGGAATTTTGAGATATCCCTTGGAAAGACCTTGCCTTGGAGAGCCTGGA
CACTAACAAATTCTACACAAATTGCTCTTCAAAATACGTTGACTGGATAACTCTGAGAAA
CACATCTAGTAAACTGAAATAAGCAGAGCATCAAATTAAACAGACAGAACCGAAAGCTTA
TATAAATGCTCAGAGTTCTTATGTTATGCTTACATGTAACATGAAATCAGAAA
ACAGGGAAATTTCATTAAAATATTGGTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T): 1
MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKKLRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGSLANI PRVREIHLENNKLKKIPSGLPEL
KYLQIIPLHSNSIARVGVNDFCP TVPKMKKS LYS AISL FNNPVKY WEM QPAT FRCVLSRMSV
OLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

101230 101231 101232 101233 101234

FIGURE 3

CGGAGCGCTGGCGGACCGCTGGGCCGCGCACCGCCCCGGCCGCCCTCCGCCTCCGCACTCGGCCCTCC
CTCCCTCGCCCGCTCCCGCCTCCCTCCCTCCCTCCCGCCAGCTGTCCCGTTCGCGTCATGCCGAGCTCC
GGCCCCGCGCCGCCCGCTGCTGCTCCCGGGCTGCTGCTCGGCTCCGGCCGGCCGCCGCCGCCAGA
GCCCGCCCGTGCCTGCCCATCGGCTCTGAGAAAGGAGCGCCTGCCCGTCCGGAGCGCAGGGCTGACCTTCGGCGG
GAAGGCTCATGCTCTGGACAGACGCTGGCACCCGGACCTAGGGCAGGCCATTGGGGTGTATGCCCTCGCTGTG
CGCCCTGCAGGGCCCTCAGGGGCTGCCCTACCAAGGGGCTGGCAGGGTCAAGCTGCAAGAACATCAAACAGA
GTGCCCAAACC CGCCGGCTGTGGCAGCGCCCTGCTGCCGGAGCTCTGCCAGACCTGCCAGGCCCGGAGCGCAG
CAGTTGGAGCGCCAGCGCAGGGCTGTCTTCGAGTATCCGGGAGCCGGAGCATCGCAATTATAGCGACCG
CGGGAGGCCAGCGCTGAGAGCGGGCCCTGGTACAGGCCACAGGACTTCGTGGCGCTGTGACAGGGCCAG
GTGCGAGGGGTGGCACGAGCCAGTCTCGCTCTGGCTCTAGCCTCTATCTCTATCTCAAGCGGCT
GGACGCCCTCAAGGATCGCTCTCAGACTCCAACTGGCAGTGCTTGTGAGCACCTGCGACGCCCAACCA
AGATGGCCCTGGTGTGGGGTGGCGGGCAGTCCTCGGTTGTCTCTGCGCTCTTAGGGCAGAACAGCTGCA
TGTGGCACTGTGACACTCACTACCCCTTAAGGGAGGCTGTGGGCCCTCATCCGACCCGGGCTGTGCG
AGAGACCTTCAGTGCCTCTGACTAGAAGGCCCCACAGCGCTGGGGCATCACCTGCTCATCT
CAGTACACAGAGGACTCTTGATTTTGCTCTTCCAGGGCTGTGAAACCCAGGAGTGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAAGGGGAGCTACTCGAGAACCTCAGGCCAATGCTTCGCCA
GGAAACAGGCTTGTGAGGTGCTGCCAACCTGACAGTCAGGAGATGGACTGGCTGGTGTGGAGCTGCA
GATGGCCCTGGAGTGGCCAGGCCAGGGCTCAGCATGAGCACATIGCTCGAGAACAGCTGCGACAGT
CTTGCAGAAAGTGTCTTTGTGGGCTGTGATGCCCTGATCCAGTCAGACGGGTGCTGCCGCTAGCCAGCTCAC
GCTGCTAGGAAAATGGCTCTGACTATCAGGTCAGAAGTGGTGGAGGACAAGCAGTGGGGTGTGCCATGACACT
GGAGACCAAGCCTCAGGGAGGGATCAGCGCAGTCCTGCTTGACCATGCGTGCAGCAGGGACACAC
GCCGCTGGGATCTGCCCTGGGTGGTGCCTGAGGGCTCATATGCTGTCAGAACATGAGCTCTCTGAAACGT
GGGCACCAAGGACTTCCCAGCAGGAGCTTCGGGGCACGTCAGTGGCTGCCCTGCCCCTACTGTGGGCTAGGCC
CATGACAGCGCTGGCCCTGGCCCTAGCAGGGACCTGGTGTACCCCTGTGAGAACAGCAGGCCAGCAG
CTGGCTTCTCTGGATACCCACTGTACCTGCACTATGAAGTGTGCTGGCTGGCTTGGGCTTGGGCTCAGAACAGG
CACTGCTACTGGGACTCCCTGGGCCCTGGAGAACCGGGCTCGCAGGGCTCTGAGGGATTCTATGGCTC
AGAGGCCAGGGTGTGGTGAAGGACCTGGAGGCCAACCTGCTGCCACCTGGCAAAGGATGCTCCCTGT
GATCACCAAGGGTAGCCCCAGAGGGAGCTCGAGGGCAGTGCACATAGCCAACCAATGTGAGGTTGGCG
ACTGGCCTGGAGGG
TGTGTCCTGCTCTCCGGGCCCTAGCGCCCGCAACACTGGTGTCTGGCGGCCAGAACCCACACATG
CTTCTTCGAGGGGAGCAGCGCCCCACGGGCTCGCTGGGCCCTAACACTGACCCGCTCTGCTCATCTGCAC
CTGGCAGAGGAGCAGGCTGGCACCCCCCTAGTGGCCGGTGGTGTGCCACCGCCAGCTGCCACCCGGTGCAGGCTCC
CGCACAGTGTGCCCTGTGGCTTGAGAACAAAGATGTCAGAGACTTGGCAGGGCTGCCAAGGAGGGGGACCC
AGAGAGGGCTGTCTATTGTGACGGAGCTGGCAGGGCTGGCGGGCAGGGGTAACGGCTGGGACCCCCCTTGTGCCCC
CTTGGCTTAATTAAAGTGTGCTGCTGACCTGCAAGGGGGGCACTGGAGAGGTGCACTGTGAGAACGGTGCAGT
TCCCCGGCTGGCCTGTGCCAGGGCTGTGCTGCAACCCACCGACTGCTGCAACACTGTGTCAGTGGGCTGG
GGCCCACCCCCAGCTGGGGGACCCATGAGGGTGTGGGCCCCCTTTGGAGAGATGAGCTGTATCACCTGCAAGATGTGGGAGG
GGTGGCTCACTGTGAGCGGGAGTACTGTGCACTGTCTGTGCTGGCTGGGGAGAGAGTCAAGGCTCTGGGTT
CCGCTGACGCCAACCGGG
GGGAGCAGCCAGGGGCAAGTGCACCAAGGAGGATGGGGCTGAGCTGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
GCATTCTCTGTGGGAAAGGGCAACTGGCTCTGTGCTCTGTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGG
CCACAGCTCACAAAGGGGGAGGGCAGGGAGCTGGGGCAGACCGAGGGTCAAGGCCACTCAAGTCTGCCACCC
TCGGGCTCTGTGCTGTGGAGCCCCACCCCTTCTCTCTGTACATAATGTCAGTGGCTTGTGGGATTTTAATT
TCTTCACTCACGACCAAGGGCCCCGACACTCACCTCTGTGCTGCCCTGAGCTGAGGAGAGTCATTATTGGAGAG
TTTGTATTATAAAACATTCTTTCTAGTCAAAAAAAAAAAAAA

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHPD LGQPFGV MRCVLCACEAPQWGRRTRGPGRVSKNIKPECPPTACGQPRQLPGHCQT
C PQERS SSER QPSGLSFEYPRDPEHRSYSDRGE GAER ARGDGHTDFV ALLTGP RSQAVAR
ARV SLLRSSLRFSISYRRLDRPTRIRFS DNGS VLF EHPAAPTQD GLVCGVWRAV PRLS RL
LRAEQLHVA LVTLTHPSGEVWGPLIRHRAA ETFS AITLLEGFPQQGVGGITLLTLS DTED
SLHFLLLFRCLLEPRSGG I LTQVPLRLQI LHQGQ LLLRE LQAN VSAQEPG FAEV LPNLT VQEMD
WLVLGELQMALE WAGR PGLR ISGHIAARKSCDV LQS VLGAD ALIPV QTGAAG SA SLTLLGN
GSLI YQVQV VGT S SEVVA MLET K PQR DQRT VLCH MAGL P QGHTAV GICPGLGARGAHML
LQNE LF LNVG T KDF PDGE LRGHVA ALPY CGHSARHD TL PVP LAGA LVLPV KSQA GHAWLS
LDT HCHL HYVE VLLA LGGG SE GTVTAH LLG PPGT PGP RLLKGF YGSEA QGVVKD LEPE LLR
HLAKGMASLM ITTKGSPRGELRGQVHIANQCEVGLR LEAAGAEGV RALGAPDTASA APPVV
PGLPALAPAKPGGPGRPRDPNTCFEGQQRPHGARWAPN YDPLCSLCTCQR RTVI CDPV VCP
PPSCPHVQAPDCCPVC EKQDV RDLFGLP RSRDPGEGCYFDGDRS WRAAGTRWHPV VVPPF
GLIKCAVCTKG GTGEV HCEKV QCP RLACA QP VRVN PTD CCKQC PVGSGAHPQLGDPM QADG
PRGCRFAGQWPFESQWHPSVPPFGE M SCITCRCGA GVPHC ERDCS LPLSCSGKESRCCS
RCTA HRRP PETR TDPE LEKA EG S

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GGCGGGAGCAGCCCTAGCGGCCACCGTCGCTCTCGCAGCTCTGTCGCCACTGCCACCGCGCGCGCGTCACTGCG
TCTCTGGCTCGCCTCCCGGCCCTCCGGCGGGCATCGCAGCCCCGCCGCCAGGGCAGCTCCCTGGCAACCCGGTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGCGAGGGGGCCCGAGGGCAGCTCCCTGGCAACCCGGTGC
CCGGCCCTCTGCTGCGCCCGCGCGAGGGCAGCTGGCTACAGCTGCACCTGCCCGGCCGGATCTCG
AGCCCGGACCCGAGCACCCGGCCCGCGAGGGCAGCTGGCTACAGCTGCACCTGCCCGGCCGGATCTCG
CCAACTGCCAGCTTGTGAGATCCTGTGCGAGCAACCCCTGTGACCATGGCAACTGAGCAGCACAGCA
GCAGCAGGGATGGCTACCTCTGCAATTGCAATGGAGGGTGAAGGGTCCAATCTGTAACAGGGCACTTCCAGTC
TCCCAGCACTGGCTGACCGAATCATGGCACGGCACGCTTACGCTGTTCTGACTCAGAGGCTGACA
AAATCTGCTCGCTCTCAGGCAACGGTACACTGCCAACCTGGCAGCGAAAACAGGGAGAAATGGTGA
TGAAAATGGGATCAAGTGGAGGGATCCGGAGATATTGGCAGGGATCTGAAGGGTCCAATCTGTAACAGC
GTCTGGTATCTTGAAGTGCACAGAACACTCTGCAAGTTCAGCTGAAGATTGCCAACCTGCCACTGTTTGC
TCTGGAAGGTCAAGGCCAACGGATTCAAAGCTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTCAGGCTT
CAGGGGGACTGGCTCTGGAGGAGATGCTGCTGGCTTGGAAATACTTATTTGGTTTGTGAAAGTATTCTG
TGACTAAGTCTATTGTGCTTGGCTTAATCTGTGTTGAAGGTGAGCAGCTGTGTCGGGGAGAGTCAG
CAAATGACTGGAGTGTTCAGGAAAAGGAAAATGACCAACGAAGGGTCAAGAGGCAACTTTCTGTACCTGT
AGGGAGCAGTAGCTGGGACTTCTGTGAGAAGTACAGCTGCTGGAGAAAACCTTGGCAGGGAAAACAGCGAGCT
GTATTGATGCAATTGAAAAGCAAGATGGGAGCAATTCACTGTGTTGGCTTCTGTGTTATACTGGAGAGCTT
GCCAGTCAAGATTGATTAAGTCTGCACTTACGCCATCAGCAAAATGGGAGCAACATGCAATTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTCTGGATCTGCTGTGAGAAGAAAAGGTGAGCCCCCTGGCTCTGCTCG
GCCAGAACACGGCACCGCCTGCTATGGAGCCTGGTACACTTACCTCTGCAACTGAGCCCCGGCTTCACAGGGCGA
CTCTGTGCCAGCTATTGACTCTGTGCCCTCACGCCCTGTGCTCATGGCACGTGCGCAGCGTGGCACAGCT
ACAAATGCCCTCTGTGATCCAGGTTACCATGGCCTTACTGTGAGGAGGAATAATGAGTGCCTCTGGCCAT
GCCCTGAATGCGACGCCAGGACCTCTGGTATGGCTATGAGTGTGCTGGCAGAATACAAGAACAC
ACTGTGAAATTGTCAAGGATCCTGCCGCTACGCTGCTGTGAGGAGCCACCTGTGACAGCGAGCCCTGA
ATGGCAGCTGATCTGTGACCCGGTTTACAGGTGAAGAGTGCAGACATTGACATAAATGAGTGCAGTAACC
CCTGCCACCATGGGAGCTGGCTGCCAGGACCCATGGTATAACTGCCACTGCCGATGGTTGGTGGAG
CAAACGTGAGATCACCTCCATGAAGTCCGGGACATGGGGAGAGGCTCACCAACATGCCACGCCACTCCC
TCTCATCATCATGAGGCCCTCTGTTGGCTTACATCTTGTGATCATCTGTGATCTGGGGATTGGCGCA
TCAGCGCATGGATCATCAGGCCATGCCGCTATGGAGGTTCTACACTGCCAGCATGCCAGACAGCG
AGTTCACTGGCATTCAGGATCATCCGGCATGGCAGGTTGGAAAAGAATCCGGCTGCAATGTGATGTGA
GCCCTCATGCCATGAAGATTACAGTCTGTGACAAACCCCTGGTCAACTGATTAAAAGTAAAGATTGT
CTTTTTGGATTATTTTCAAAAAGATGAGATACTACACTCATGGTAAATTATTTTAAGAAAATAAAAGCTTAA
GAAAATTTAAAATGCTAGCTGCTCAAGGTTTCAGTAAATTTAAGAATCAATTCTGCACTTGTGTT
GAAAAATTTAAAACAAAATTGTGAAACCTATAGCAGTGGTTAAATGTACCTTCAGCTCTAAACTGT
GTGCTCTACTAGTGTGCTTCTTCACTGTGAGCAGTACAGCAGAGACCTATCAGCAGAGACCA
GAATAAGTCTAATCAAGGAGAGTTCTGTGAGCTTCTGAGTGGCGCTTCTGAGTAGAGTGTGAAAACAC
GTAACCTGAGCATATGATGATATAAGTGTATACCCGTTACTTAAAAGAAGTCTGAAATGTTGTTGGAAA
AGAAAAGTAAATTACTATCCATACCGGATGAAATTAGCCTTACTTGTGATCTGGTCAAGGGTAAAGTAAAC
TTATTCGACTGTGTTGTGAACTTTGTGAAACATTCAGTGGCTTGTGATCTGGTCAAGGGTAAAGTAA
TCGAACATGGGCTCAAAACATCTAAGCAGAAAAGGCTAGCGAGGCAAATTCTGATGATTGATTTGA
TTCTTTAAAAGTCAGGGTTCTATTTGAGTAAATTAAATTACATTGAGTTGTTGTGCAAGGGTAG
TAAATGTAAGAGAGTACTGGTTCTTCAGTAGTGTGACTATTCTCATGTCAGCTTGTGTT
TTTGTGGCTGTTGATGATGTGCTTCTGTGATTCTGCTAATTTCAACCATATTGAAATAATGTGATC
AAGTC

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQP RRAQAPGA QQLL PALALL LLLGAG PRG S LANP VPA APLS A PGP CAAQ PCRN GG VCT SR
PEP DPQHPA PA GE PG YS CTCP AGIS GANC QLVAD PCAS NPCH HGNC SSSSS SDGY LCIC N
EGY EGPN CEQ ALPS L PAT GWT ESMAP RQL QPV PA T QEPD KIL PRS QAT VTL PTW QPKT GQ KV
VEM KWDQ VEVIP DIACGN ASNS SAGGL VSF EV PQNT SVK IRQ DATAS L ILL WKV TAT GF Q
QCS LID GR SVT PLQ ASGG L VLLE EML ALG NNH FIG FV ND SVT KSIV ALR LTV KV STC VPG
E SHAN DLECS GKG KCTT KSE AT FSCT CEE QYVG TCE EYD A QRK PCQ NN AS CID AN E KQ D
GSN FTCV CLPG YTG ELC QSK IDY C ILD PCRN GAT C ISSL SGFT CQC PEG YFG SACE EK VD PC
A SPC QNNG T CYV DG V HFTC NCSP GFT GTC A QL ID FCAL S PC A HGT CR SVG T SYK CLCD PG
YH GLY CEE EYNE CLS APCL NAAT C RD L VNG YEC V CLAE YKG TH CELY KDP CAN V SCL NG ATC
DSD GLN GT C IAP GFT GE CD ID IN ECD S NPCH HGG SCLD QPN GYN CHCP HGW VG ANCE IHL
QWK SGH MAES L TNM P R HSL YII I GAL CV AF ILM L II LIV GIC RIS RIE YQ GSS R PAY E FYN
CRS ID SEFS NAI ASIR HAR FG KK SR PAMY DV SPI AY ED YSP DD KPL VTL IKT KDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTCAGGGGACTGGTCCCTGGAGGAGATGCTCGCCTGGGAATA
ATCACTTTATTGGTTTGTAATGAATCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCAAGCGTCAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTGCCAAAACAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGAGCAATTACCTGTGTTGCCCTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGAG

FIGURE 8

CTCTGGAAAGGTACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTCAGGCTTTAGGGGGACTGGTCCTCCTGGAGGAGATGCTGCCTGGGAATA
ATCACTTTATTGGTTTGTAATGATTCTGTGACTAAGTCTATTGTGGCTTGCGCTTAAC
CTGGTGGTGAAGGTACGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACACGAAGCCGTCAGAGGCAACTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTCTGTGAAGAATACGATGCTGCCAGAGGAAACCTTGCCAAAACAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTACACCTGTGTTGCCCTCC
TGGTTATACTGGAGAGCTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGAG

FIGURE 9

GCTGAGTCTGCTCCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCA CGCTGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCAGCACCACGGGCCTGCAAGAGCAGGCACGGGCC
GATGCGGGACTTCCCGCTGTCGGACGCCACA CGACCTGCCCCCTGGTCTAAGGCAGGTTT
ACCA GAAAGGGCTACAGGATGTTAACCTGCGAATTTCAGCTACGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGCGCCAGTTCTGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCCCTCACCCCTGGAGCAGATTGACCTCATGCCGATGTGCGCT
CCTATTCTGAGCTGGAGCTTGACCTCGCTGGCTAAAGCTCTGAACGACACTCAGAAATTGCC
TGCCTCATCGGTAGAGGGTGGCACTCGCTGGACAATAGCCTCTCCATTTACGTACCTT
CTACATGCTGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGCAGAGA
GCTCCGCTAAGGGCTCCACTCCTCTACAACAACATCAGCGGCTGACTGACTTTGGTAG
AAGGTGGTGGCAGAAATGAACCGCCTGGCATGATGGTAGACTTATCCATGTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTCTCCCCTCGCTGCC
GGGGTGTGCAACAGTGTCTGGAAATGTTCTGATGACATCTGCGACTTCTGAAGAAGAAC
GGTGGCGTGTGATGGTGCTTTGTCCATGGGAGTAATACAGTGCAACCCATGCCAATGT
GTCCACTGTGGCAGATCACTTGACCAACATCAAGGCTCTATTGGATCCAAGTTCATGGGA
TTGGTGGAGATTATGATGGGCCGCAAATTCCCTCAGGGCTGGAAGACGTGTCACATAC
CCGGCTGTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTCAGGGTGTCT
TCGTGGAAACCTGCTGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAATGGC
AAAGCCCCCTGGAGGACAAGTCCGGATGAGCAGCTGAGCAGTCCCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACACTACTGAGATTCCCATACA
CTGGACGCCAAGTTACAGCCAAGTGGTCACTCTCAGAGTCCCTCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTTGATGACCCAGTTAGTCC
TGCCAGATGCACTGTAGCAAGGCCACAGACACCCCAAAAGTCCCCCTGTTGTGCAGGCACA
AAATTTCTGAAATAATGTTTGGACATAG

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLA CLIGVEGGHSLDNSLSILRTFYMLGVRYLTILTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGM MVDSLHVSDA VARRA LEVSQAPVIFSHSAARGVCNSARNV PDDILQ
LLKKNGG VVMVSLSMGVIC QCNPSANV STVADHF DHI KAVIGSK FIGIGGDYDGAGKFPQGLE
DVSTYPV LIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEE NKWQS PLEDKF PDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLA VVATFPV LILWL

TOTERG 11544+60

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAAACCTATAAATATTCCGGATTATTCAACCGTCCCACCATCGGGCGGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCGTGATGCCGGACTTCCGCTCGGACGGCCAC
AACGACCTGCCCTGGTCTTAAGGCAGGTTTACAGAAAAGGGCTACAGGATGTTAACCTGCG
CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGTTAGAGATGCCCTCGTGGGCCAGT
TCTGGTCAGCTATGTGCATGCCAGACCCAGGACGGGATGCCCTCGCCTCACCTGGAG
CAGATTGACCTCATGCCGATGTGCTCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAAATTGGCCTGCCTCATGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTACATGCTGGAGTGGCTACCTGACGCTC
ACCCACACCTGCAACACACCCCTGGGAGAGGCTCCCTAAGGGCTCCACTCTTACAA
CAACATCAGGGGCTGACTGACTTTGGTGAGAGGCTGGCAGAAAATGAACCGCTGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGCCACGGCGGGCTGGAAAGTGTACAG
GCACCTGTGATCTTCTCCACTCGGCTCCCGGGGTGTTGCAACAGTGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTCTGAAGAAGAACGGTGGCTCGTGTGATGGTGTCTTGCCATGG
GAGTAATACAGTGAACCCATCAGCCAATGTTGTCACGTGGCAGATCACTTCGACCACATC
AAGGCTGTCACTGGATCCAAGGTTATGGGATTGGTGGAGATTATGATGGGGCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCACACATCCCGTCTGTAGAGGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCGTGGAAACCTGCTGCGGGCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCTTGAGGAGACAAGTTCCGGATGA
GCAGCTGAGCAGTCTCCACTCGACCTCTCACGCTCGGTGAGAGACAGAGTCTGACTT
CAGGCCAGGAACACTGAGATTCCACACTGGACAGCCAAGTTACCAAGTGGTCA
GTCTCAGAGTCTCTCCCCCACCTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGA
ACTCCTGGGGGACCGTCAGTCTCTCCCCCAAAACCAAGGACACC

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T) : 5
MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRRLRDGLVGQAQFW SAYVPCQTQDRDALRLTLEQIDLIRRMCA SYSELELVTSAKALND
TQKLA CLIGVEGGHSLDN SLSILRTFYMLGVRYLTLTHTCNT PWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNR LGMMV DLSHVSDA VRA LEVS QAPVIFSHSAARGVCNSAR NVPDDILO
LLKKNGGV VMVSLSMGVICQCNPSANVSTVADHFDIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLI EELL SRGWSEEELQGVLRGNLLRVFRQVKVQEE NKWQS PLEDKF PDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLP AKWSVSESSPHPD KTHCPCPAE LLGGP
SVFLFPPP KPKDT
```

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCGGCCCTCCCGCGCCCGGCCCTGCGTCCCGCGCC
CTGCGCCACC CGCGAGCGCAGCCGCCGCGGCCCTGGCCCGGCCCTGCGTCCCGCGCC
GCCGGCGCCGGGCCCCCGGCCAATCCGCGCGGCCGCGGCCCTGGCCCGGCCCTGCGTCCCGCGCC
GCTGCTGCTCTGCGTCCTCGGGCGCGAGCGGATCAGGAGCCACACAGCTGTGATCA
GTCCCCAGGATCCCACGCTCTCATCGGCTCTCCCTGCTGGCCACCTGCTCAGTGCACGGA
GACCCACCAAGGAGGCCACCCCGAGGGCCTACTGGACCCCTAACGGCGCCGCTGCCCCC
TGAGCTCTCCCGTGTACTCAACGCCCTCACCTGGCTCTGGCCCTGGCCAACTCAATGGGT
CCAGGCAGGGCTGGGGACAACCTCGTGTGCCACGCCGTGACGGCAGCATCCTGGCTGGC
TCCTGCCTCATGTTGGCTGCCCCCAGAGAAACCGCTAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGGCGCTGGACGCCAGGGGCCACGGGGAGACCTTCTCACACCA
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACAC
ACAGTGGGGCCCCACTCCTGCCACATCCCAAGGACCTGGCTCTCTTACGCCCTATGAGAT
CTGGGTGGAGGGCACCAACCGCCTGGGCTCTGCCGCTCCGATGTACTCACGCTGGATATCC
TGGATGTGGTGACCGACGGACCCCCCGCCGACGTGACGTGAGCCCGTGGGGGCTGGAG
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTAACGGATTCCCTTTCAAGCCAA
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGAGCATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCTGAAACCCGCCACCGTGTACTCGTGCAGTGC
TGCAACCCCTTGGCATCTATGGCTCAAAGAAAGCCGGATCTGGAGTGA GTGGAGGCCACCC
CACAGCCGCTCCTACCCCGCAGTGA GGCCCGGGCCGGCGGGCGTGCAGTGC
GGGGCGGAGAGCCGAGCTGGGGCCGGTGC GGCGCGAGCTAACAGCTTCTGGCTGGCTC
AAGAAGCACCGCTACTGCTCCAACCTCACGCTTCCGCTCTACGACCAAGTGGCGAGGCC
GCAGAAGTGCACAGACCCGCAACCAAGGAGCAGGGGATCTGCCCTGGCGAGCGGGCA
CGGGCAGAGGGCTCTGCCAGATAAGCTGTAGGGCTCAGGCCACCCCTGCCACGTGGAGA
CGCAGAGGCCAACCCAACTGGGGCACCTCTGTACCCCTACCTCAGGGCACCTGAGGCCAC
CCTCAGCAGGAGCTGGGGTGGCCCTGAGCTCAACGGCATAACAGCTCTGACTCCACGT
GAGGCCACCTTGGGTGACCCCAAGTGGGTGTTGAGGGTTGGTTGAGTTG
CTAGAACCCCTGCCAGGGCTGGGGTGA GAGAAGGGAGTCATTACTCCCCATTACCTAGGGCC
CCTCCAAAAGAGTCCTTTAAATAAATGAGCTATTAGGTGCTGTGATTGTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAA

FIGURE 14

><ss.DNA38113
><subunit 1 of 1, 422 aa, 1 stop
><MW: 46302, pI: 9.42, NX(S/T): 6
MPAGRRGPAAQSARRPPPLPLLCLVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGLRLPELSRVLNASTLALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLRLWYQQDNTCEE
YHTVGPHSCHIPKDIALFTPYEIWVEATNRQLGSARSDVLTLDILDVTTDPPPVDHVSERVGG
LEDQLSLVRWVSPPAKDFLFQAKYQIRYRVEDSVWDKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGPGGGACEPRGGEPPSSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILPSGRRGTARGPAR

TOKESO "454545660

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

FIGURE 16

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pI: 9.52, NX(S/T): 1
MKFLLDILLLPPLLIVCSLESFVULKFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFLATQDPQIEKTFEVNVNLAHFWTKAFLPAMTKNNGHIVTVASAAGHVSVPFLAYC
SSKFAAVGFHKTLDELAALQITGVKTCLCPNFNTGFIKNPSTSLGPTLEPEEEVVNRLMH
GILTEOKMIFIPSSIAFLTTLERILPERFLAVLKRKISVVKFDAVIGYKMKQA
```

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GACTAGTTCTTGGAGTCCTGGGAGGAGGAAGCGGAGCCGGCAGGGAGCGAACCAAGGACTG
GGGTGACGGCAGGGCAGGGGCGCTGGCGGGGAGAAGCGCAGGGCTGGAGCACCAAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGGCCGGAGGGGGACT
GCGAGAGGACCCCGCGTCGGGCTCCGGTGCCAGCG**TAG**GAGGCCACTCCTCGTCTGC
TGCTCCTGGCCTGGCGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCAGCCTCTGC
CCGGGCACCCGGCCTTCAGGCACGCCGGCCACCATGGCAGCCAGGGCTGCCGGCG
CGATGGCCGCGACGGCCGCGACGGCGCCGGGCTCCGGAGAGAAAGGCAGGGCG
GGCGGGACTGCGGGACCTCGAGGGGACCCGGCGCGAGGAGGGCGGGACCCCGCGGG
CCCACCGGGCTGCCGGGAGTGCTCGTGCTCCGGATCCGCTTCAGGCCAACGCTC
CGAGAGCCGGGTGCCTCCGCGTCTGACGCACCCCTGCCCTCGACCGCGTGTGGTAACG
AGCAGGGACATTACGACGCCGTACCGCAAGTTCACCTGCCAGGTGCCCTGGGTCTACTAC
TTCGCCGTCATGCCACCGCTACCGGCCAGCCTGCAGTTGATCTGGTGAAGAATGGCA
ATCCATTGCCCTTTCCAGTTTCGGGGGTGGGCCAAGCCAGCCTCGCTCGGGGG
GGGCCATGGTGAGGCTGGAGCTGAGGACCAAGTGTGGGTGCAGTGGGTGTGGTGA
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTCTCCGGATTCTGGTGTACTCGA
CTGGCACAGCTCCCAAGTCTTGCT**TAG**TGCCACTGCAAAGTGAGCTCATGCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCACTCCAGGAGGGCTGGCCCCCTGGA
GTGAATGACTAGGGAGGTGGGTAGAGCACTCTCCGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCCATCAGGTCTGGCAGCATGGGCAGTGCTGGATTCTGCCAACGCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCACGGT
GGGGTGCTCTCTGGCTGCTGGATCCTCCCCACCCCTCCTGCTCCCTGG
GCCGGCCCTTTCTCAGAGATCACTCAATAAACCTAAGAACCCCTCATAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 18

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592
><subunit 1 of 1, 243 aa, 1 stop
><MW: 25298, pI: 6.44, NX(S/T): 0
MRPLLVLLLLGLAAGSPLLDDNKIPSLCPGHPGLPGTPGHGSQGLPGRDGRDGRDGAPGAP
GEKGEGGRPGLPGPRGDGPGRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPL
FDRVLVNEQGHYDAVTGKFTCQVPGVYYPAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQWWQVGVGDYIGIYASIKTDSTPSGFLVYSDWHSSPVFA
```

Signal sequence.

amino acids 1-15

TOTEBO™ Information

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCC**AT**
GCTGCATCCAGACCTCCCTGGCGGGGCATCTCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCCACCTGGCAGAGGTGTGGCACCCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAAACAGGAAGGAGAGTTCCTGCTCCCTCCCTGCACAAACCGCTGCGCAGCTGGTCCA
GCCCTGCGGCTGACATCGGAGGCTGGACTGGAGTGCACAGCCTGGCCAACTGGCTCAAG
CCAGGGCAGGCCCTCTGTGGAATCCAAACCCCGAGCCTGGCATCCGGCTGTGGCGCACCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCCTTGTGAAGTGGTCAG
CCTATGGTTGAGAGGGCAGCGGTACAGCCACGGGAGAGTGTGCTCGAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGCCACCTCAAGCCAGCTGGCTGTGGCGGCAC
CTGTGCTCTGAGGCCAGACGCGATAAGGCCTTGTGCTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCACGGGAAGACAATCATCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGGACCATGAGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGCAGATACTGCCAAGTGCAGGTGCAGCCTGCAGTGTGTC
ACGGCCGGTCCGGGAGGAGGTGCTGCGTCTGTGACATCGGCTACGGGGAGCCAG
TGTGCCCCAACGGTGCATTTCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGAACACTTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTGCCCTCTATCTGGCCGC
CTGGAGACCACCAAGGGTGAAGTGCAGCTGACACTTGCAGGACAGGAACTTCTGGATCGGCT
CACCTACAAGACCGCCAAGGACTCTCCGCTGGGCCACAGGGGAGCACCAGGCCCTCACCA
GTTTGCCCTTGGGAGCCTGACAACCAACGGGCTGGTGTGGCTGAGTGCCTGCCATGGGTT
GGCAACTGCGTGGAGGCTGAGGCTTCAGCTGCCCTCAACTGGAACGACAGCGCTGCAAAC
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCAGGGTCT**C**
GAGGCCTGACCACATGGCTCCCTGCCCTGCCCTGGAGCACGGGCTGTGCTTACCTGTCTGC
CCACCTGTGGACAAGGGCAGGTTAAAGACCATGCTCATGTCAAAGAGGTCTCAGA
CCTTGCAAAATGCCAGAAAGTGGGAGAGAGGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTAGAAGAAGCTGGGCCCTGCCCTGCTTTGATGGGAAGATGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTCCACCTGGCCAGAC
CCTGTGGGGCAGCGGGCTTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG
CTGAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
MLHPETSPGRGHLLAVLALLGTTWAEVWPPQLQEQQAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSDSLALQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG
NWEVNGKTIIPIYKKAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH
CHCPCPGYTGRYCVQRCSLQCVHGRFREEECSCVCDIGYGAQCATKVHFPFHCTDLRIDGDC
FMVSSEADTYYRARMKCQRKGVLQAQIKSOKVQDILAFYLGRLETTNEVTDSDFETRNFwig
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNVCVELQASAAFNWNDQRCK
TRNRYYICQFAQEHIISRWGPGS

Signal sequence.
amino acids 1-26

Transmembrane domain.
amino acids 110-124

N-glycosylation sites.
amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 45-49

N-myristoylation sites.
amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 204-215

EGF-like domain cysteine pattern signature.
amino acids 249-261, 280-292

C-type lectin domain signature.
amino acids 417-442

FIGURE 21

CGGACGCGTGGCTGGGCGTGC~~AAGCGTGT~~CCGCCGGTCCCCGAGCGTCCC~~GCGCCCT~~
CGCCCCGCCA**ATG**CTCCTGCTGCTGGGCGTGTGCGTGGGCTGTCCCTGTGTGTGGGTCGA
GGAAGAGGCCAGAGCTGGGCCACTCTCGGAGCAGGATGGACTCAGGGTCCCAGGCAAG
TCAGACTGTTGAGAGGCTGAAAACAAACCTTGTGACAGAAATTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCCCTCACTACGGTTCTGTGACAGGATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGAGCTTTCATACCAAACITCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACACAGAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCGATTCCCAGAACAGGACAAAGGCCCTTTTCTGAGTTATGAGGAGCTTC
TGAGAGGCCCTGGGCAACTACGAGCACAGCATCAGCTGCGGCCAGCAGCTGTCGGG
AGGCTGAGCGTGGACGTGAATATCTGTGAGAGCGCGGCCATCGCATCCCTGGAGGTGTCGC
GCTTCACAAACAGCAGGCGAGGGCGATGGCGCGGGGAAGATGATTCGGGCTCCCCAT
CTACTGTCAATTACCAAATGAAACATTCGCAACATAATTAAACCTACTGTAGTACAA
CAAGCCAGGAAITGCCAGAATGGAATTGGAGACTTATCATTAGATATGACGTCAATAG
AGAAACAGAGCATTGGGACATCCAGGTTCTAAATGCTTATTTGTGCACTACTGTCTTA
AAGACCTTCCTCTTACCCAAGAATGTTGATTCTGCTGACAGCAGTGTCTTATGGTG
GGAACCAAACCTCGGCAGACCAAGGATGCCCTCTTCAACATTCTCATGACCTCGGACCCCA
GGACCGTTTCAGTATCATTGGATTTCACAACGGGATAAAAGTATGAGGACCACTTGTAT
CAGTCACTTCAGACAGCAGGATGGGGAGTGTACATTCCACCATATGTCACCCACTGG
GGCACAGACATCAACGGGCCCTGCAGGGGCCATCAGGCTCTTCAACAAAGTAGTGGCCA
CAGTGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGGCCACGG
TCGGGGAGACGCACACCCCTCAAGATCTCAACAAACACCGGAGAGGCCCGGGAGGCCAAGTC
TGCATCTTACCATGGCATCGCAACAGCAGTGGACTCTCAGGCTGCTGGAGAAACTGTC
GGAGAGCTGGCCTCACAGCGCGTGCAGCAGGAGGAGGAGCAGGCTGCGAGCTCATCG
GGTTCTACGATGAAATCAGGACCCGCTCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGTGAGGGCACCAGGACCTGTTCTCAACGGCTGGAGATCATCAT
TGCAGGAGACTGGTGGACAGGAAGCTGGATCACCTGCAGCTGGAGGTACCCGCCAACAA
GTAAGAAATTCATCATCTGAAAGACAGATGTGCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCAAGGCGTGGAGGCGATGGAGAGGGGACACCAACCCACATCGAGCT
CTGGAGCTACCTCACACAAAGGAGCTGTGAGCTCTGGCTGCAAAGTGACGATGAAACGG
AGAAGAGCGGCTCGGCAGCGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC
TTCACCTCATGAAGCTGAGGGGCCGGTCCCACGATGGATGGCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCTGCGAGGAGCTGGCACGCAGC
CAGGACCTTGCTCAAGAAGCCTAACTCCGTCAAAAAAACAAACAAAACAAAAAAAGA
CATGGGAGAGATGGTGTGTTTCTCCACCACTGGGATACGAT**GA**GAAGATGCCACCT
GCAAGCCAGGAAGACGCCCTCACAGACACCATGTCGTGGCACCTGATCTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAATGTGTTTGTAAAGCTAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
<MW: 77400, pi: 9.54, NX(S/T): 6
MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPQRVRLLQLRKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRKNKTTEENGKGTIEIFRASAVIPSCKDAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSRGEDDSGPPIPSTVINQNETFANIFKPTVVQQAR
IAQNGILGDFIIIRYDVNREQSIGDIQVNLNGYFVHYFAPKDLPLPKNVVFVLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRRIKVWKDHLLISVTPDSIRDGKVYIHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTTRRVHEBEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEIIIAGKLVDRKLDLHLVEVTASNNSKKFIILKTDVPVRPQKAGKDVTG
SPRPGGDGEGDTNHIERLWSYLTTKELSSWLQSDDEPEKERLRRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEAHGMSAAMGPEPVVQSVRGAGTQPGLLKKPNSVKKQNKTKKRHGR
DGVFPPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGTGCCGACATGGCGAGTGTAGTGCTGCCAGCGGATCCAGTGTGCGGC
GGCAGCGGGCGCGCGGCCCTCCCGGCTCCGCTTCTGCTGTTCTCTCCGCCGCG
CACTGATCCCCACAGGTGATGGCAGAAATCTGTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCAAGTCATAAAGAGTGACGACTCTGTGATTCACTGAA
TCCCACAGGCAGACCATTATTCAGGGACTTCAGGCCCTTGAAGGGACAGCAGGTTCACTGAA
TGCTGAATTCTAGCAGTGAACCAAAGTATCATTGACAAACGTCCTAATTCTGATGAA
GGAAGATACTTTGCCAGCTATACCGATCCCCACAGGAAAGTTACACCACATCACAGT
CCTGGTCCCACACGTAATCTGATGATCGATCATCCAGAAAGACACTGGGTGGAAGGTGAGG
AGATTGAAGTCACACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGTTCAAA
GGGAACACAGAGCTAAAGGCAATCGGAGGTGAAAGTGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGACAAGGAGCAGTGGGTCCCACTGATCTGCCAGGTGG
AGCACCCCTGCCGTCACTGAAACCTGCAAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTCAAGTGAACCTTACACGCTTAACCCGGGAAGGGGACCGCTTGA
GTTAACATGTGAAGCCATCGGAAGCCCCAGCCTGTGATGGTAACTGGGTGAGAGTCGATG
ATGAAATGCCCAACACGCCGTACTGTCGGGCCAACCTGTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTCAAACATAGTGGGGAAAGCTCACTGGATT
TATGCTGTATGTATACGATCCCCCACAACATACCTCCCTCCACAACAACCACCA
CCACCAACACCACCAACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTGTGGCGGTGGTGGTGGTGGCCT
GCTGTGCTGTCATCATTCTGGGGCGTATTTGCCAGACATAAAGGTACATACCTTCACTC
ATGAAGCCAAGGAGCCGATGACGCAGCAGACGCAGACAGCTATAATCAATGAGAAGGA
GGACAGAACAACTCCGAAGAAAAAGAAAAGACTTCATCTAGATCAGCCTTTTGTGTTCAAT
GAGGTGTCCAACTGGCCCTATTAGATGATAAAGAGACAGTGATATTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
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QVNKSDDSVIQLLNPNRQTIFYFRDFRPLKDSRFQLLNFSSSELKVSLTNVISDEGRYFCQL
YTDPPQESYTTITVLPVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLTQRYLEVQYKPQVHQIQT
YPLQGLTRGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSODYMLYYDPPTTIPPTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACCGGACTCGAACGAGCTTGCTTGGGACCCAGGACCCCCCTGGGCCGA
CCGCCAGAAAAGACTGAGGCCGCGGCCCTGCCCCGCCGGCTCCCTGCGCCGCCGCCCTC
CCGGACAGAAGATGTCTCCAGGGCTCCCTCTGCTGCGCTGCTCTGCTACTGCCCT
GGGGCTGGGTGAGGGCTGCCATCCGGCTGCCAGTGAGCAGCTGCCACCCGACACGGTGGGCTGTAC
GCACTGCCGCCAGGGACACGGTGGCCAGACGTGCCACCCGACACGGTGGGCTGTAC
GTCTTGAGAACGGCATCACCATGCTGAGCAGCAGCTTGGCGGCCCTGCCAGCTGCA
GCTCTGGACCTGACAGAACAGATGCCAGCTGCCCTGCCCTGCCCTGCTGCTGG
ACCTCAGGCCAACAGCCTCTGGGCCCTGGAGCCGGCATCTTGACACTGCCAACGTGGAG
GCGCTGGCTGGCTGGTGTGGGCTGAGCAGCTGGAGGGCTCTTGAGCCCTTGCG
CAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCGAGTGGCACCTGTGATCCAG
GCCCTGGGCCCTGACGCCCTGCGGCCCTGGCCGAACACCCGACATTGCCAGCTGCCAGCC
GAGGGACTGCGGCCCTGCGCTGCCAGGGCTGGATGTGAGCACACCTAAGCCTGAGGC
CCTGGCTGGGCCACTCTGGGCCCTTCCCCCGCTGGCTGAGCTGGCAGCTGCCCAACC
CCTTAACATGCGTGTGCCCTGAGCTGTTTGGCCCTGGGTGCGGAGGCCACGTCACA
CTGGCAGCCCTGAGGAGACGCCGCTGCCACTTCCGCCAAAGAACGCTGGCCGGCTGCTCT
GGAGCTTGACTACGCCGACTTGGCTGCCAGGCCACACCAGCCACAGTGGCCACCA
CGAGGCCCTGGTGGCGGGAGCCCACAGCTTGTCTAGCTGGCTCTACCTGGCTTAGC
CCCCACAGCCGGGCACTGGGCCCCACTGGGCCCCAGCCGCCCTCACTGCCCAACC
GACTTCCCCAGGCCACTGGGCTGGCCACCTGGCCACCTGGCTCTAGCTGGCTCTACCTGG
GGACACGGGACCCACCTGGCTGCTTGTGCCCCGAAGGCTTCAAGGGCTGTACTGTGAGGC
CAGATGGGGCAGGGACACGCCAGCCCTACACCAGTCACGCCAGGCCACCCGGCTCT
GACCCCTGGGACATGGGGCTGGGACGCCACCTCCCTGGCGCTGGGCTGAGCGCTACCTCC
AGGGAGCTCTGGTGCAGCTCAGGGCTCTGGCTCATGGCAACCTATGCCAACT
AAGCGCTGGTGTGAGCTGCCACTGGCTGCTCGCTCGCTGAGTACAGGTACCCAGCTGG
GCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTGGGGCCGGGGTGCAGGGAGGGCG
AGGAGGCTGGGGAGGGCCATACACCCCCAGGCCACTCCACCCAGGCCACCCGGTACCC
CAGGGCCCCAGGGCAACTGGCTCTCATGGCCGCCCTGGCCGGCTGGCTCTGG
CGGGCTGGCTGGGGAGGGCAGCTACTGTGCGGGGGGGGGGGCATGGCAGCAGCG
CTCAGGACAAAGGGCAGGTGGGGCAGGGCTGGGCCCTGGGACTGGAGGGAGTGAAGGTC
CCCTGGAGGCCAGGCCAGGGCAAGGCAACAGAGGGGGGGAGAGGCCCTGCCAGGGCTGTGA
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCTGGGCCACTGCCAGGCCAAAGC
CCTACATCTAAAGCCAGAGAGAGACAGGGCAGCTGGGGGGCTCTCAGCCAGTGGAGATGGC
CAGCCCCCTCTGGCCACACCCAGTAAGTTCTCAGTCCAAACCTGGGGATGTGCTGAGA
CAGGGCTGGTGTGACCAAGCTGGGCCCTGGCTCTGGACCTGGCTCTCATCTGTGAG
ATGCTGTGGGCCAGCTGACGAGCCCTAACGTCCTGGCAGAGGAGTGGCTATGAGGACAGTGT
CCGCCCTGCCCTCCGACAGTGCAGTCCTGGCAGCCGGGGCCCTGCCATGTGCTGGTAAC
GCATGCCCTGGGCCCTGCTGGCTCTCCACCTCCAGGGGAGCCCTGGGGGGCAGTGAAGGAAG
CTCCCGAAAGAGCAGGGAGAGCGGGTAGGGCTGTGACTCTAGTCTTGCTGCTTTAA
AAGCGAAGGAAACAAAGAAACTGAAAGGAAGATGCTTGTAGAACATGTTTGTCTTCAAAC
AGAGACAAGGACTTGGTTGTAAAGACAAAGATGATATGAGGCCTTGTAAAGAAAAA
ATAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804
<subunit 1 of 1, 598 aa, 1 stop
<MW: 63030, pI: 7.24, NX(S/T): 3
MCSRVPLLLLPQLLALGPVGVQGCPGCGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN
GITMLDASSFAGLPGLQLLDSLQNQIASLRLPRLLLDLHNSLLALEPGILD'TANVEALRL
AGLGLQQLDEGLFSRLRNHLHLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSQLALFGDLSGLFPLRLLAAARNPFCNCVPLSWFGPVRESHTLASP
EETRCHFPPKAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPPTAPPTVGVVPQCPDCPPSTCLNGGTCHLGRHLACLCPEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLLTGLIEPVSPSTSRLVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLV
TLRLPASLAEYVTQLRPNATYSVCVMLGPGRVPEGEEACCEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAQDKGQVGPAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPGPGLQSPHLAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACGTCCCAGCTACCCCTACCCGCCCGCACC
TCCTTGCTACCCCACTCTGAAACACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTCTTCTGCTAGCCCCAAAGGCCTCCAGGAACATGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGCAGCTCTGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCCTCCGGAGCAGA
GTTCCGATGCCCTGGAAGCTGGGAGAATGGGAGAGATCCCGGAAAAGGAGAGCAGTGTC
ACCCAAAAACAGAAGAACGAGCAGCACTCTGCTCTGCACCTGGTTCCCATTAACGCCACCTCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCAAGGATATGGTGTCCGAATCAGGATGCTGGAGTTATCTGCTGTATAGCCAGGTC
CTGTTCAAGACGTGACTTACCATGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCTACACAGCT
GCTATAGCGCAGGTGTCTCCATTACACCAAGGGGATATTCTGAGTGTCTAATCCCCGG
GCAAGGGCGAAACTTAACCTCTCCACATGGAACCTTCTGGGTTTGTGAAACTGT**GATT**
GTGTTATAAAAAGTGGCTCCAGCTTGGAAAGACCAGGGTGGGTACATACTGGAGACGCCA
GAGCTGAGTATATAAGGAGAGGGATGTGCAGGAACAGAGGCATCTCCTGGGTTGGCTC
CCCGTTCCCACTTTCCCTTTCACTCCACCCCTAGACTTTGATTTACGGATATCTTG
CTTCTGTTCCCATGGAGCTCCG

FIGURE 28

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27433, pI: 9.85, NX(S/T): 2
MPASSPFLLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKHSQLHLVPIN
ATSKDDSDVTVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSVREG
QGRQETLFRCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGTVKL
```

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTTCTCTTACTTCAGAAACCGCGCTTCCGCTCTGGTCGAGAGAC
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTTGGGGGGACCTGTGGCTCGTA
CGGCCCCCACCCCTCTCTCTGCACTGCCGCTCTCCGAAGACCTTTCCCTGCTCTGTT
TCCCTCACCGAGTCTGTGATCGCCCCGAGCTGGCCGGAGGAGGCTGGCCGGAGA
TGCTCTAGGGCGGGCGGGAGGAGCGGGCCGGAGCGAGGGCCGGAGGAAGATGGC
TCCCCTGGACAGGGACTCTGCTGGTACTGCTGCTCCCTGCCTTGCCTCTGGCTGGT
CTCTGAGTCTGTGCCCCATGCAAGGGGAACAGCAGGAGTGGAGGGGACTGAGGAGTC
CTGCGCTCGGACCATGCCAGGGCTGAAGAACACAATGAAAATAACAGGCCACTCAG
GACCAGGGCTCTCTGCTTCCGGTCTTGCCTGCGTCTGTGACCCCGTACCTCCATGTACCC
GGCCACGCCCTGCCCAAGATCAACATCACTATCTGAAAGGGAGAAGGGTGACCGGGAG
ATCGAGGCCCTCAAGGGAAATATGCAAAACAGGCTCAGCAGGGCAGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCATGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCC
CTTTCTGGTGGCCGGAAAGGCCATGCCAGAACCAACTACACAGGGTGTACTTCTG
ACACGGAGTCTGTGAACCTTACGACCATCTCAACATGTTACCGGCAAGTCTACTGCTAC
GTGCCGCCCTACTTCTCAGCCTCAACGTGACACCTGGAACAGAAGGGACCTACCT
GCACATCATGAAGAACGAGGGAGGTGATCTTGTGCGCAGGTGGGACCGCAGCA
TCATGCAAAGCCAGAGCTGATGCTGGAGCTGGAGACGAGGCCAGGTGTGGTACGCC
TACAAGGGCAGCTGAGAACGCCATCTCAGCAGGGAGCTGACACCTACATCACCTCAG
TGGCTACCTGGTCAAGCACGCCAGGAGCCTAGTGGCCGCCACCTCTTCTCTGCC
ACCTTCCACCCCTGCGTGTGCTGACCCACCGCTTCCCGATCCCTGACTCCGACTC
CCTGGCTTGGCATTCACTGAGACGCCCTGACACACAGAAAGCCAAGCGATGGTCTCC
CAGATCCCGCAGCCTCTGGAGAGGCTGACGGCAGATGAAATCACCAAGGGCGGCC
GAGAACCTCTGGGACCTCCGGCCCTCTGCAACATCCTCAACTGACCCCGCAGCC
GAGACGGGGCGGGCAGGGCTCCAGGTGGCAGGCGCTCAGTCTGGAAATA
ATTAGGCAAATTCTAAAGGTCTAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTGTCTTCCAGCCAGCTGCTGGCTCCAAGAGAGAGGGCTTTCTAGTGG
ACTCTGCTTAAGGAGAGATCCAAGTAAAGCTCTGGGTGAGGGGAGGGGGGGGGGG
AAACATACCTCTGGCTTAATCTTCTTAAAGCACAGTAGGAACCTTCTGAGGGATAAGTGGACC
CTGACATCCCTGTGGCTTGCCTGCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGTGCAGGT
GATGGGGCTGGGGCCCAAGGCCAGGCCAGCTCCAGAGGGACAGCTGAGCCCTGCTTGG
TCCAGGGTGGTAGAGCAGCCGAAGGGCTCTGACAGTGGCAGGGACCCCTGGCTCC
GCCCTGAGATTTCTATGAGGGCAGAGCTCTGGTACATCATGTTGCTGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGTCTCATGCTGCCACCCCTGGCATCGCT
TTCTGTGCCCTGCCACCAAACTCAGGCCAGAAGGCCGGGGCTTGGCTCTGTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCTGTTGCTAAGCATCACCCT
CCACGTGTGTTGTTGGCAGCAAGGCTGATCCAGACCCCTCTGCCCAACTGCCCT
CATCCAGGCCCTGACCAAGTAGGCTGAGAGGGCTTCTAGGCTTCAGAGCAGGGAGAG
CTGGAAGGGCTAGAGAACCTCCCGCTTGTGTTCTCAGGCTCTGTGAGGCTCACTCAG
AGACCAAGAGTCAAGGAGAGTACACGCCAACTACCCGTGTCAGGATTCACTCTCAG
TGGGTGGCAGGAGAGGCAATAGGCCCTGTGCAATTGCAAGGACAGCTGGAGCAGGGTGC
GTGCTCCACGGTGTCTGCCCTGCCATGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCCCTCCACCCATGCCACCTGGTGTGAGGCCAGGGTCACTCTGCTACCCCTGG
CCCCAACCCCCGGCTGCCCTCTCTTCTCCCCCATGCCACCTGGTTTGACTTAACCTGC
TCTCCCTCTGGGCTGCCCTGCCGGATCTGGGCTCTTAAGTCCCTCTTTAAAGAACCT
CTGGGGTCAAGACTCTGAAGGCCAGGTTGCTGTGGGGTGTGCCGGAGCAGAGGCCACACTC
GCTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAACCTCAGAATTGTTCAAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYTQVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMELREQDQVWV
RLYKGERENAIIFSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GC GGAGC AT CGCT CGGGT CCT CGCC GAGA CCCC CGCGG ATT CGCGG TCT CCC CGGG
CGCG GAC AGAG CTG CCT CGCAC TGAT GGCG AGGG CGCC GGGT CCT CT CGAC GCCA
GAGAGAAATCTCATCTGTGAGCCTCTAAAGCAA ACTAAGACCAAGGGAGGATTAT
CTTGACCTTGAAGACAAA ACTAACTGAATTTAAATGTTCTCGGGGAGAAGGGAG
CTTGACTTACACTTTGGATAATTTGCTTCTGACACTAAGGCTGTCGCTAGTCAGAATT
GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTTCTAAGGGAAATC
AGAGGCAATGAGCCGTTATATCTAACTAAGAAGACTGCATTAAATTCTGCTGTTAAC
AAAAAAACATATCAGGGACAAGCATGTAACCTGATGATCTCGACACTCGAAAAACAGCTA
GACAACCCAATGCTACCTTTCTGCTCCAACAGGAAAGCCTGCACTGAAACAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCCATCTTGACCAGAAATTGCAAG
CCAAGAGTTACCCAGGAAGATTCTCTTACATGCCAATTTCACAAGCAGTCACTCCCC
TAGGCCATCATCACACAGATTATCAGGCCAACCGATATCTCATGGAGAGACACATTCT
CAGAAGTTGGATCTCAGTCACCTGGAGAAAATTTAAAGATGGATGAAGCAAGTGC
GCTTCTGCTATAAGGAAAAGGCCATTCTCAGACTCACATTTCCTGATCAAGAAA
TAGCTCATCTGTCGCTGAAAATGTGAGTGCCTCCAGCTCGGAGTTGCTTCTCCA
CATACCACCTCGCTACTCCAAAGGCCAACCTCTACCCACCAATGCTTCAGTGACACC
TTCTGGGACTTCCAGCAAGCTGGCACCCAGCTCCACAGTCCACCTGTAACCCACTGCACTTCTC
AGCCTCCACGCCCTCATCTCAGTTTACAGGAAACTCTAACCTTGAAACACAGGAAATGTGATAACCTA
GCTACAACAGCAGTCTGACTACCACCTTCAAGGCACTACGGACTCGAAAGGCAGCTTGA
AACCATACCGTTACAGAAATCTCAACTTAACCTTGAAACACAGGAAATGTGATAACCTA
CTGCACTTCTATGTCAATGTGGAGTCTCCACTATGAAATAAAACTGCTTCTGGAAAGGT
AGGGAGGCCAGTCAGGCCAGTTCTCCAGGGCAGTGTCCAGAAATCAGTACGCCCTCC
ATTGAAAATGGCTCTATCGGGTCCCTGCTTGGTCTCTGGTCTCTGGAGACAGGTCTT
TCGTCCTCTGGTAGAATCTTCTGGAAACTCTCCGAGGAAACCTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTGGTCTCTTAATTCTT
TAGTAACCGAAGGCCAAATGCAATGAGTTCTGCTGACTTGTACTCTAGCAGGAGGTG
TATTTGAAAGACAGGAAATGCCCTCTGCTTCTGGTCTCTGGAGACAGGTCTT
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTGGCTCTCACCGCAACCTCCGTCTC
CTGGGTTCAAGCGATTCTCTGCTCAGCCTCTAAGTATCTGGGATTACAGGCATGTGCC
CCACACCTGGGTGATTTGTATTTTAGTAGAGACGGGTTTCACTGGTCTGGGATTACAGG
GTCTCAAACCTCTGACCTAGTGTACCCCTCTGCCCTCCAAAGTGTCTGGGATTACAGG
CATGAGGCCAACAGCTGCCCTCTGTTTATGTTGGTTTGTGAGAAGGAATGAAGT
GGAACCAAATTAGGTAATTGGGTAATCTGTCTCTAAATATTAGCTAAAACAAAGCT
ATGTAAGGAAATAAAGTATAATTGCCATATAAAATTCAAAATTCACTGGTTTATGCAA
GAAACAGCTTAGGACATCTAGGTTCCAATTCACTCACATTCTGGTCCAGATAAAATCAAC
TGTGTTATCAATTCTAATGGATTGTTCTTTATGTTGATTCTGGATCCTTAAACTTATT
CCAGATGTGTTCTCCAATTAAATTTGAAATAAACTTTGTTACTCAA

FIGURE 32

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T) : 6
MFFGGEGSLTYTLVIICFLTRLASQNCNLKKSLEDVVIDIQSSL SKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
S LTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTVTSPQPTT LISTVFTRAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTA SWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSES LRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

CGGGCACCTGGAAG**ATG**CGCCCATTGGCTGGTGCCTGCTCAAGGTGGTTCGTGGCTTC
GCCTCCTTGTGCTGGTACCTGCTCGCAGAGCTCATTCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGAGAGGCCGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAATGTGACCCTGGACTCCCTGCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAACAGTACGCCAAATCTGTTGAGGATAACCTACTTATGGG
AGAACAGCTGGAAATGTTGCGAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
ATGTGACAGCAACAGATGTTTGTATGATGAGGCGATAACTCTGGACCGATGACAAG
TTTATTCAAGGTGCTGCCAAATCCCTGCTCTCATGGTGCACCTATGACGACGAAAGCAC
AAGACTGAATAACGATGCCAGAACATGCCATAGAACGACTTGGAAAGTAAAGAAATCAGGAACA
TGAAATTCAAGGTCTAGCTGGGTATTGAGCAGCAAAGGCTTGGAACTCCCTTCCGAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACACAGATATTCTGGCTGGCTGCAGA
GATCCAGATAGAAGGCTGCATAACCCAAAGAACGAAG**TGA**CACTGCAGGGCTCTGAGTAAAT
GTGTTCTGTATAACAAATGCAGCTGGAAATCGCTCAAGAATCTTATTTCTAAATCCAACA
GCCCATATTGATGAGTATTTGGTTGTTGAAACCAATGAACATTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAAGTATTTATGTAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAA

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777  
><subunit 1 of 1, 235 aa, 1 stop  
><MW: 25982, pI: 9.09, NX(S/T): 2  
MRPLAGGLKVVVFVVFASLCAWYSGYLALELIPDAFLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNVYVTGNVTAT  
RCFDMDYEGDNGSPMTKFIQSAAPKSLLFMVTDGGSTRLNNDAKNATEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQQREKINHSDAKNNRYSGWPAEIQIEGCPKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125